AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

I claim:

1-22 (Cancelled)

23. (Currently Amended) A method of recruiting an RNA splicing ~~processing or translation~~ factor to a target RNA species, the method comprising:

providing a nucleic acid molecule having a first domain capable of forming a first specific binding pair with a target sequence on the target RNA species, and a second domain capable of forming a second specific binding pair with an RNA splicing ~~processing or translation~~ factor, and

contacting the nucleic acid molecule with the target RNA species and with the RNA splicing ~~processing or translation~~ factor.

24-25. (Cancelled)

26. (Currently Amended) A method ~~or a use~~ according to claim 23 wherein formation of the first specific binding pair and the second specific binding pair recruits the RNA splicing ~~processing or translation~~ factor to an RNA splicing ~~processing or translation~~ site on the target RNA species to effect RNA splicing ~~processing or translation~~ at said RNA splicing ~~processing or translation~~ site.

27. (Cancelled)

28. (Currently Amended) A method according to claim 23 ~~27~~ wherein the target sequence is within 100 nucleotides of an RNA splicing ~~processing or translation~~ site on the RNA target species.

29. (Cancelled)

30. (Currently Amended) A method or a use according to claim 23 for increasing the level of splicing at a specific splice site on a target RNA species, wherein the first domain of the nucleic acid molecule forms a specific binding pair with a target sequence close to the specific splice site on the RNA species~~, and wherein the second domain forms a specific binding pair with an RNA splicing factor~~.

31. (Previously Presented) A method according to claim 30 wherein the specific splice site is a cryptic splice site or a mutated splice site.

32. (Currently Amended) A method according to claim 23 for increasing the level of incorporation of a specific exon in a pre-mRNA species into a mature mRNA species, wherein the first domain of the nucleic acid molecule forms a specific binding pair with a target sequence in the ~~specific exon of the~~ pre-mRNA species~~, and wherein the second domain forms a specific binding pair with an RNA splicing factor~~.

33. (Currently Amended) A method ~~or a use~~ according to claim 23 ~~30 or 32~~ wherein the RNA splicing factor is selected from the group consisting of: SR proteins, SR-related proteins, and hnRNP proteins, ~~CELF proteins, STAR proteins,~~ and any RNA~~, RNA-protein complex~~ or protein that stimulates splicing activity.

34. (Previously Presented) A method according to Claim 23 which is performed in an *in vitro* cell-free system.

35. (Previously Presented) A method according to Claim 23 which is performed in an *ex vivo* cellular system.

36. (Previously Presented) A method according to Claim 23 which is performed in an *ex vivo* tissue-based system.

37. (Previously Presented) A method according to Claim 23 which is performed *in vivo* in the human or animal body.

38. (Currently Amended) A method according to claim 23 of treating a condition characterised by defective or undesirable RNA splicing in an individual, the method comprising administering to the individual a nucleic acid molecule as defined in claim 23 wherein the ~~having a~~ first domain is capable of forming a specific binding pair with a target region of a defectively spliced target RNA species ~~and having a second domain that forms a specific binding pair with an RNA splicing factor~~, and wherein the target region of the target RNA species is sufficiently close on the RNA species to the site of defective or undesirable splicing for splicing at the site to be enhanced by the action of the splicing factor.

39. (Cancelled)

40. (Previously Presented) A method according to claim 38 wherein the RNA splicing factor is selected from the group consisting of: SR proteins, SR-related proteins and hnRNP proteins, and any RNA or protein that stimulates splicing activity.

41. (Previously Presented) A method according to claim 38 wherein the defective RNA splicing is caused by a mutation at the site of defective splicing.

42. (Previously Presented) A method according to claim 38 wherein enhanced exonic incorporation is desirable at the site of undesirable RNA splicing.

43. (Previously Presented) A method according to claim 38 wherein the condition is selected from spinal muscular atrophy, breast cancer, Becker muscular dystrophy and β-thalassaemia.

44-60. (Cancelled)

61. (New) A method according to claim 23, wherein the nucleic acid molecule is from 13 to 100 nucleotides in length.

62. (New) A method according to claim 23, wherein said first domain of said nucleic acid molecule attaches to said target sequence of said RNA target species by means of complementary base pairing.

63. (New) A method according to claim 23, wherein said second domain forms a second specific binding pair with an RNA splicing factor selected from the UsnRNP group of RNA splicing factors.

64. (New) A method according to claim 63, wherein said second domain forms a second specific binding pair with U1 or U2 snRNP.

65. (New) A method according to claim 23, wherein said second domain is not complementary to the target RNA species.

66. (New) A method according to claim 23, wherein said nucleic acid molecule comprises at least one modified nucleotide.

67. (New) A method according to claim 66, wherein said at least one modified nucleotide is chemically modified to enhance stability or uptake by a cell.

68. (New) A method according to claim 66, wherein said at least one modified nucleotide is selected from the group consisting of a 2'-*O*-methyl derivative of RNA, a phosphothiorate modification, a morpholino modification and a phosphoroamidate modification.

69. (New) A method according to claim 23, wherein said second domain comprises the sequence CAGGUAAGU.

70. (New) A method according to claim 23, wherein said second domain comprises the sequence AGGAGGACGGAGGACGGAGGACA.